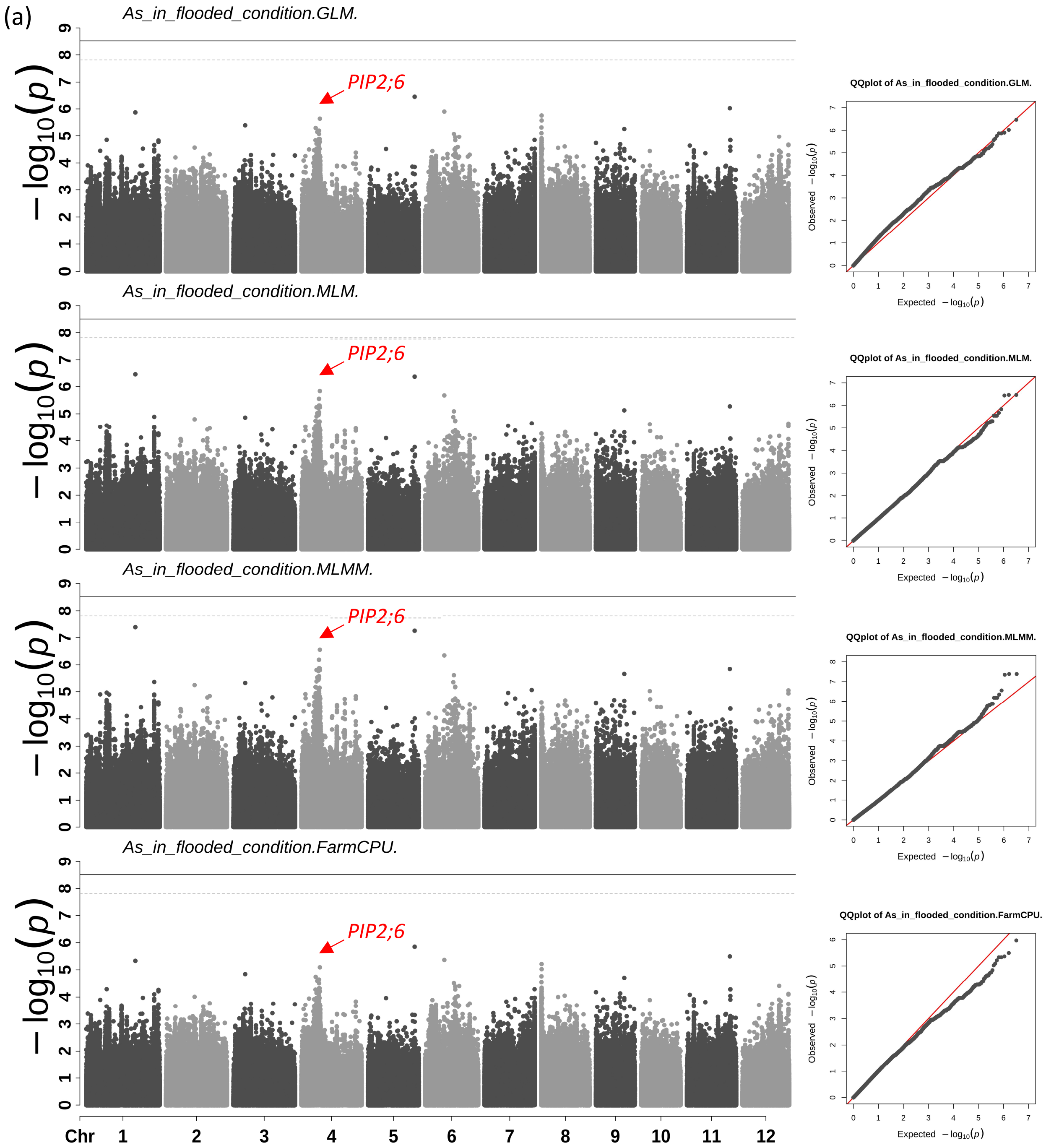
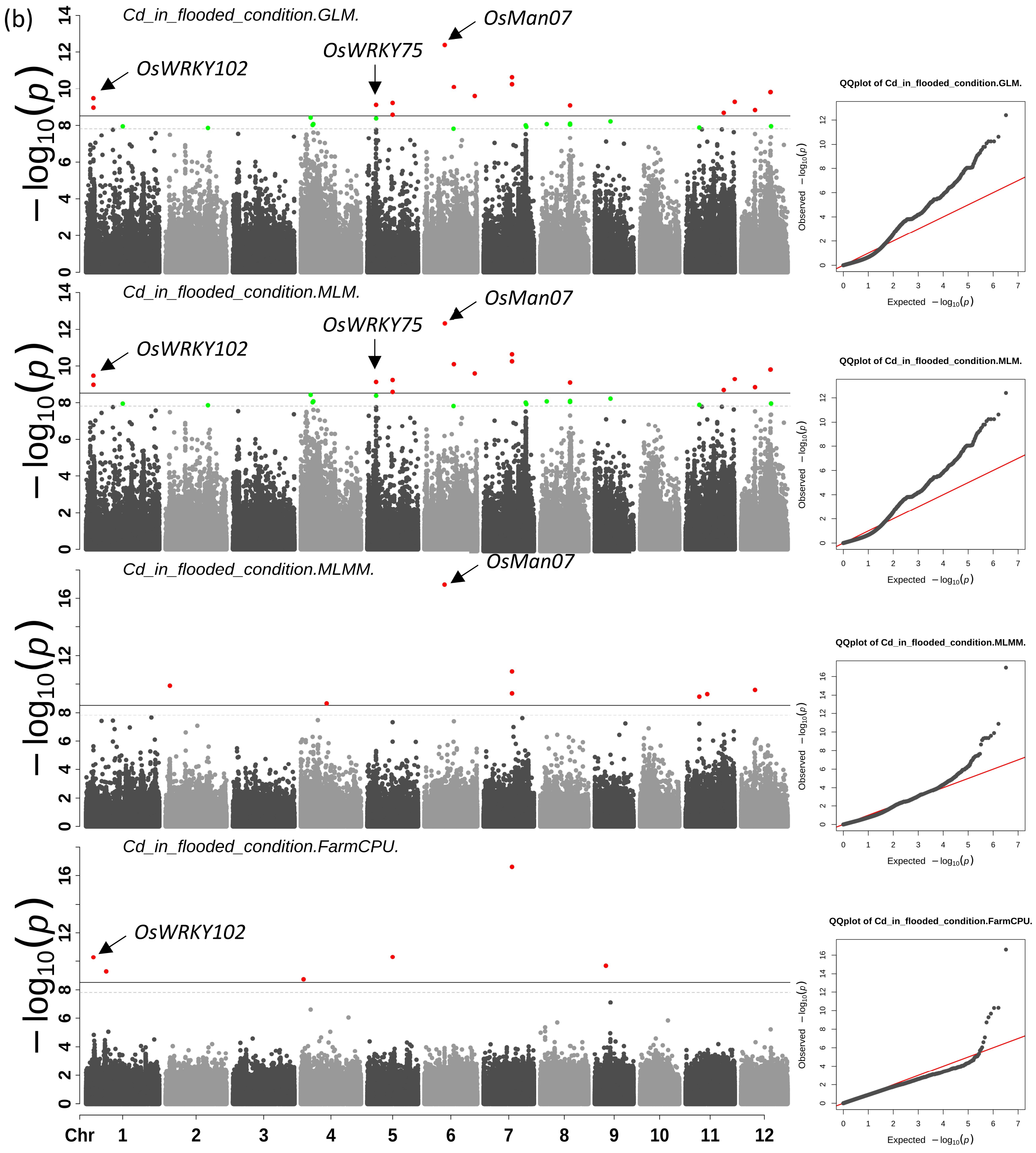
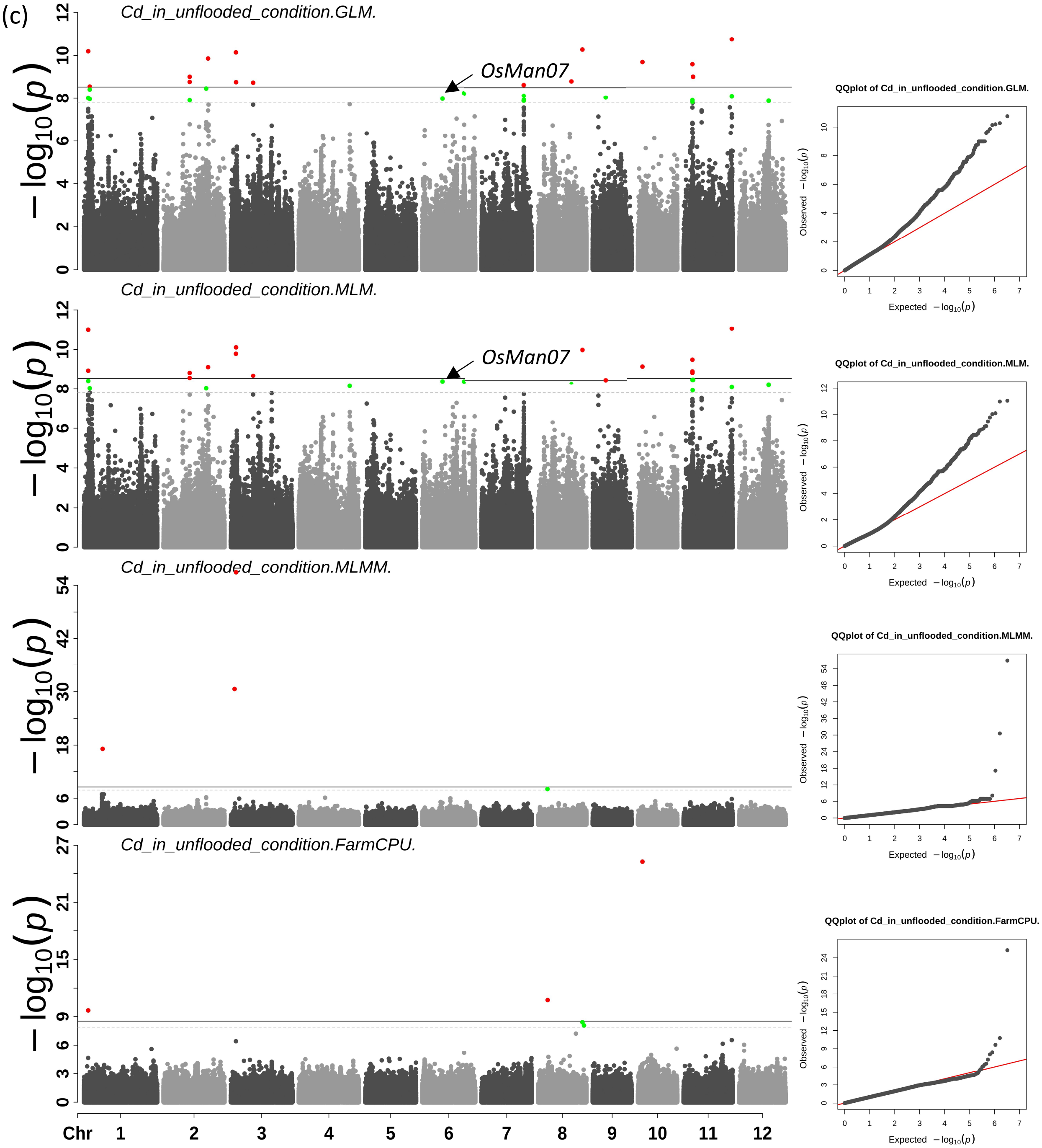


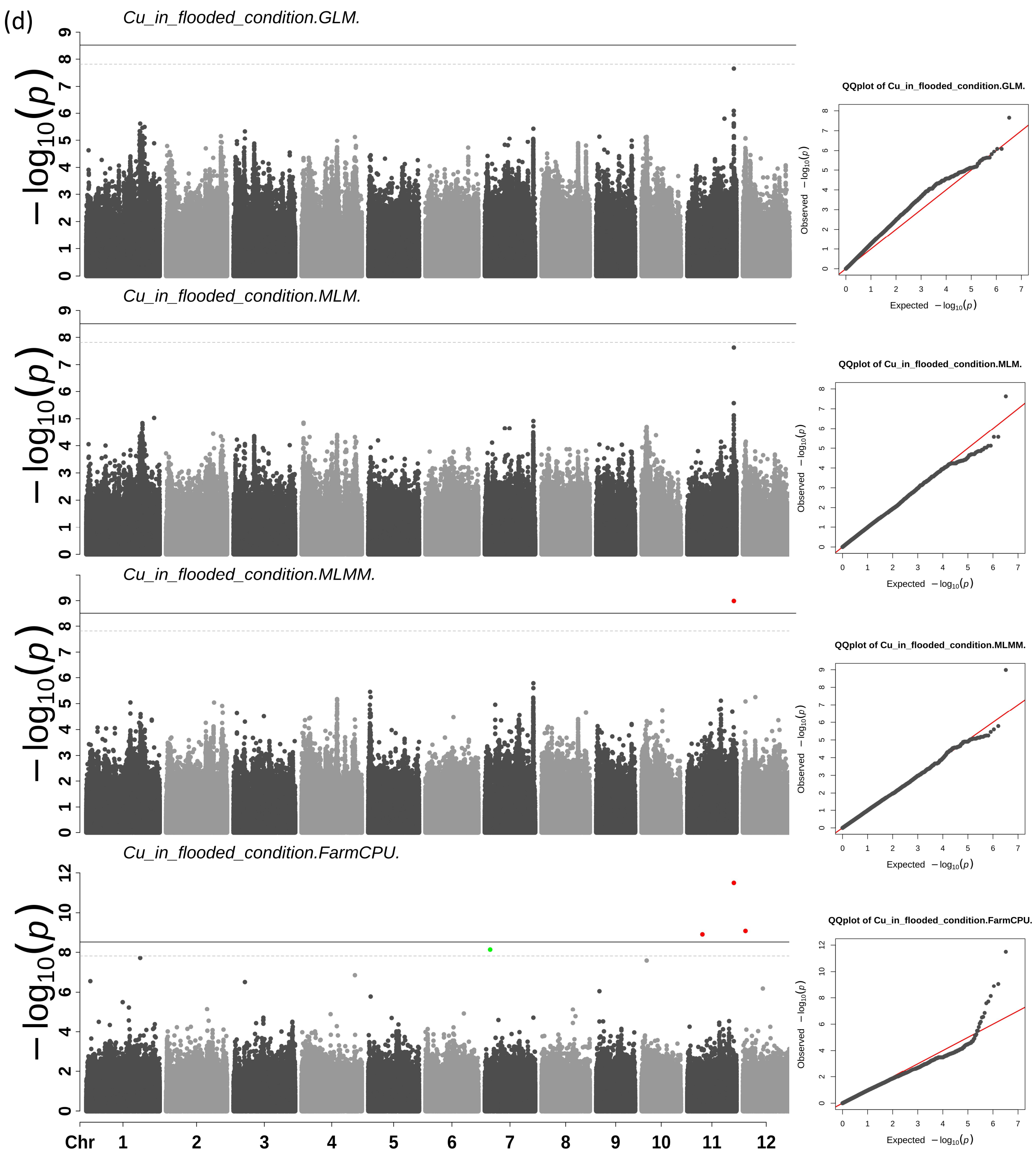
Supplementary Figure 2 (a) Genome-wide association analysis for As with GLM, MLM, MLMM, and FarmCPU methods (left) in flooded condition. Quantile-quantile plot of each model (right). Red arrow indicates published gene, black arrow indicates candidate gene. The horizontal dot grey line and green dots indicate the Bonferroni-corrected significance thresholds and SNPs at −log10(*P*) = 7.81. The horizontal solid grey line and red dots indicate the Bonferroni-corrected significance thresholds and SNPs at −log10(*P*) = 8.51.



Supplementary Figure 2 (b) Genome-wide association analysis for Cd with GLM, MLM, MLMM, and FarmCPU methods (left) in flooded condition. Quantile-quantile plot of each model (right). Black arrows indicate candidate genes. The horizontal dot grey line and green dots indicate the Bonferroni-corrected significance thresholds and SNPs at −log10(*P*) = 7.81. The horizontal solid grey line and red dots indicate the Bonferroni-corrected significance thresholds and SNPs at −log10(*P*) = 8.51.

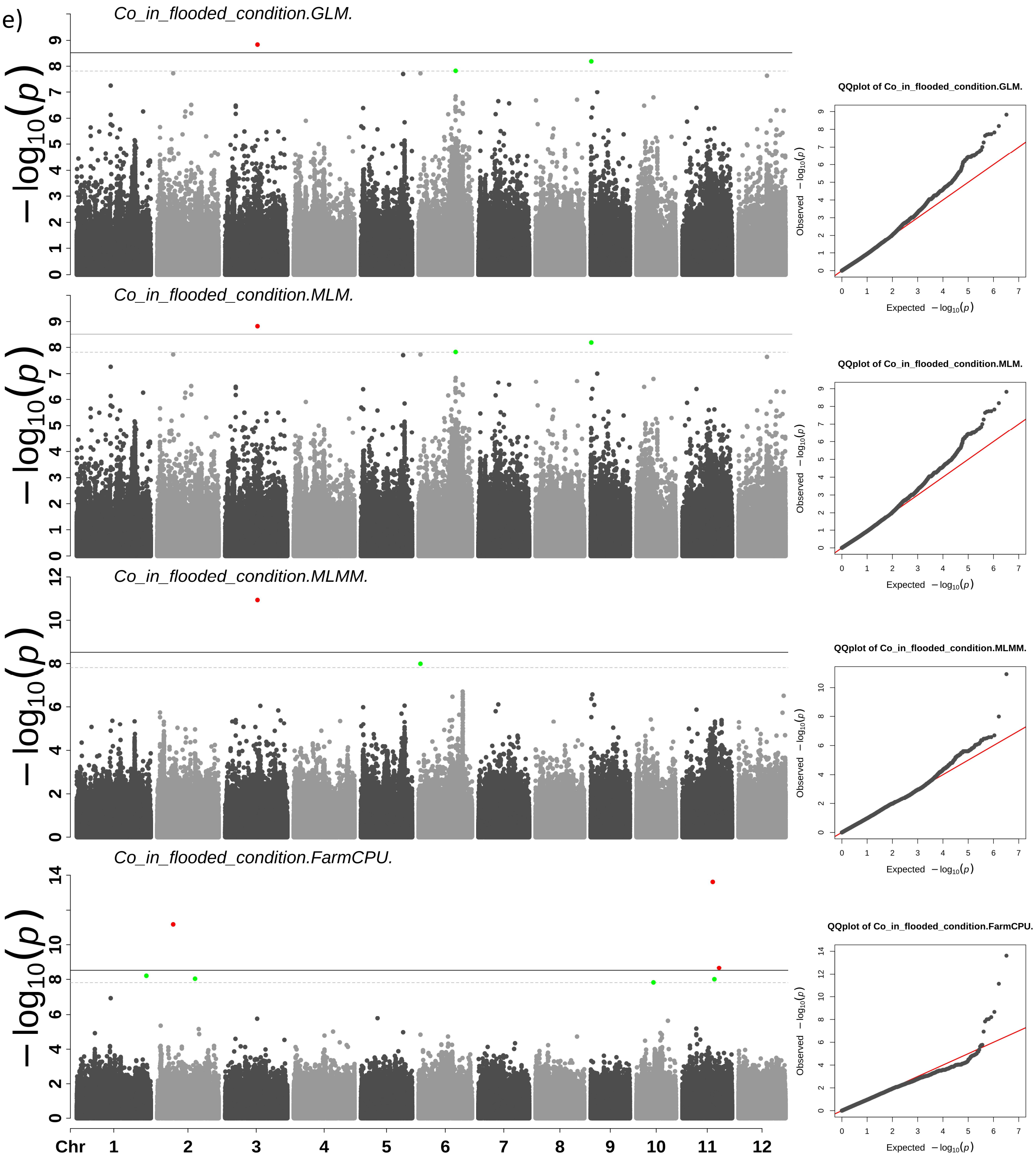


Supplementary Figure 2 (c) Genome-wide association analysis for Cd with GLM, MLM, MLMM, and FarmCPU methods (left) in unflooded condition. Quantile-quantile plot of each model (right). Black arrows indicate candidate genes. The horizontal dot grey line and green dots indicate the Bonferroni-corrected significance thresholds and SNPs at −log10(*P*) = 7.81. The horizontal solid grey line and red dots indicate the Bonferroni-corrected significance thresholds and SNPs at −log10(*P*) = 8.51.



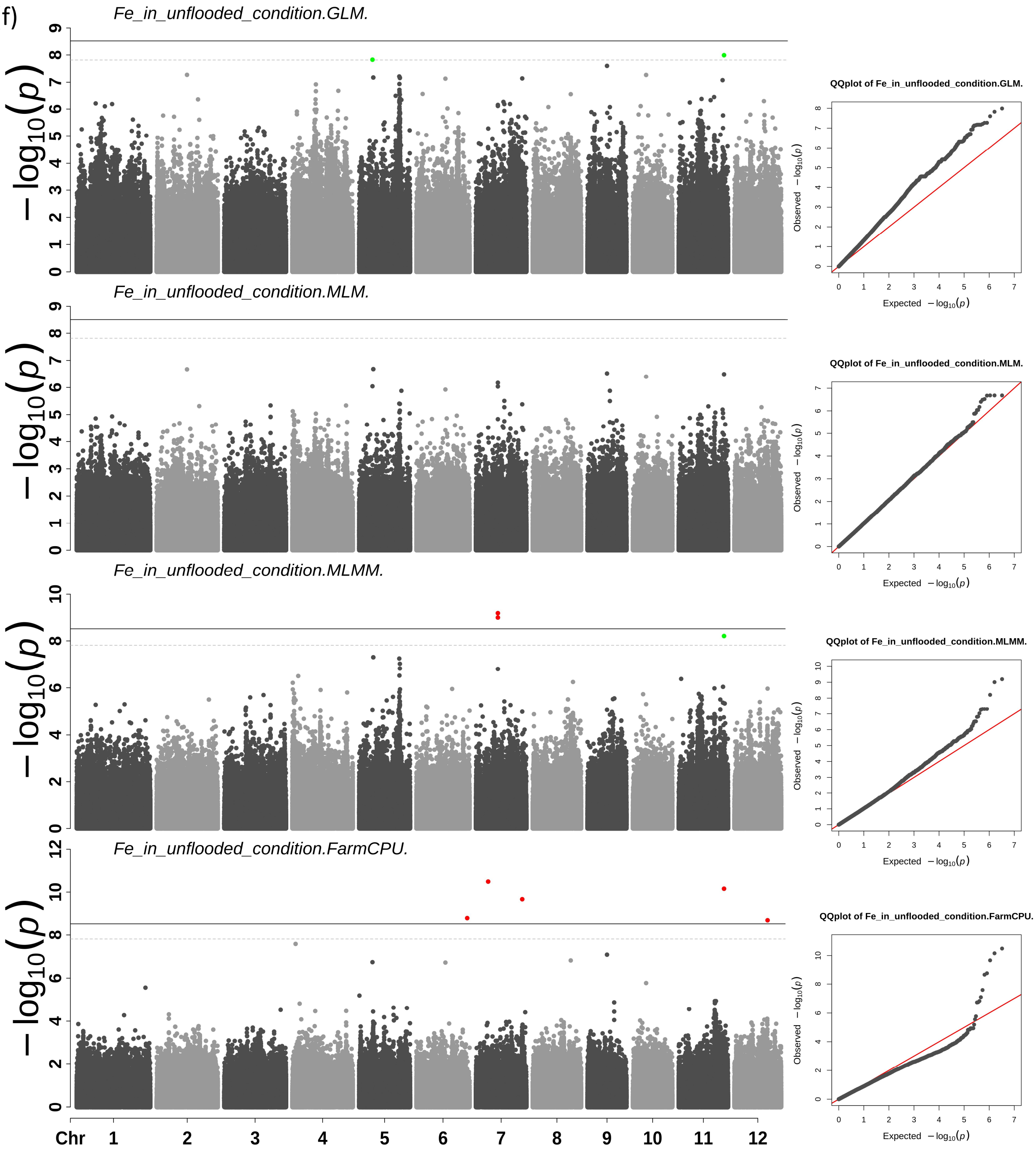
Supplementary Figure 2 (d) Genome-wide association analysis for Cu with GLM, MLM, MLMM, and FarmCPU methods (left) in flooded condition. Quantile-quantile plot of each model (right). The horizontal dot grey line and green dots indicate the Bonferroni-corrected significance thresholds and SNPs at −log10(*P*) = 7.81. The horizontal solid grey line and red dots indicate the Bonferroni-corrected significance thresholds and SNPs at −log10(*P*) = 8.51.

(e)

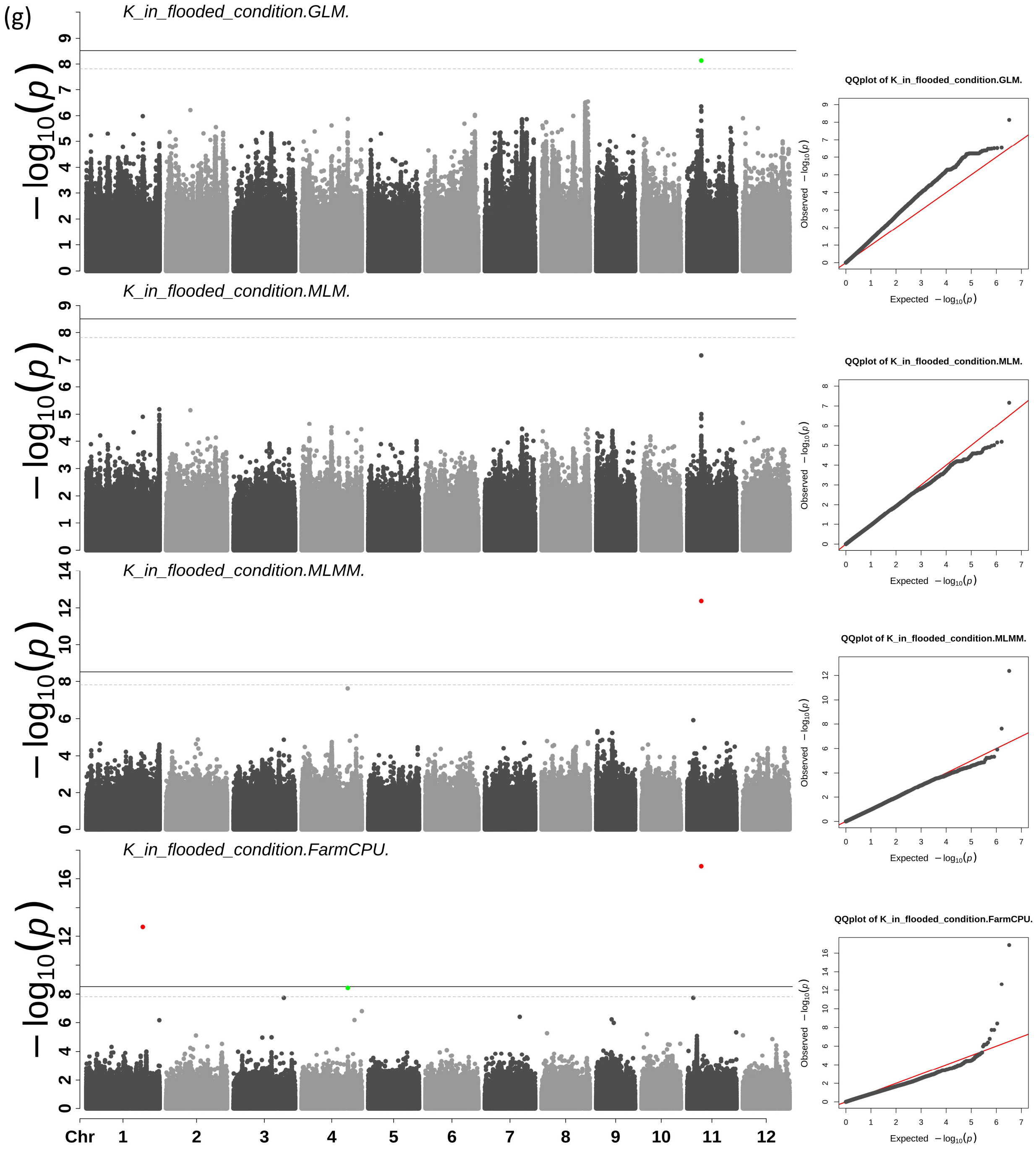


Supplementary Figure 2 (e) Genome-wide association analysis for Co with GLM, MLM, MLMM, and FarmCPU methods (left) in flooded condition. Quantile-quantile plot of each model (right). The horizontal dot grey line and green dots indicate the Bonferroni-corrected significance thresholds and SNPs at −log10(*P*) = 7.81. The horizontal solid grey line and red dots indicate the Bonferroni-corrected significance thresholds and SNPs at −log10(*P*) = 8.51.

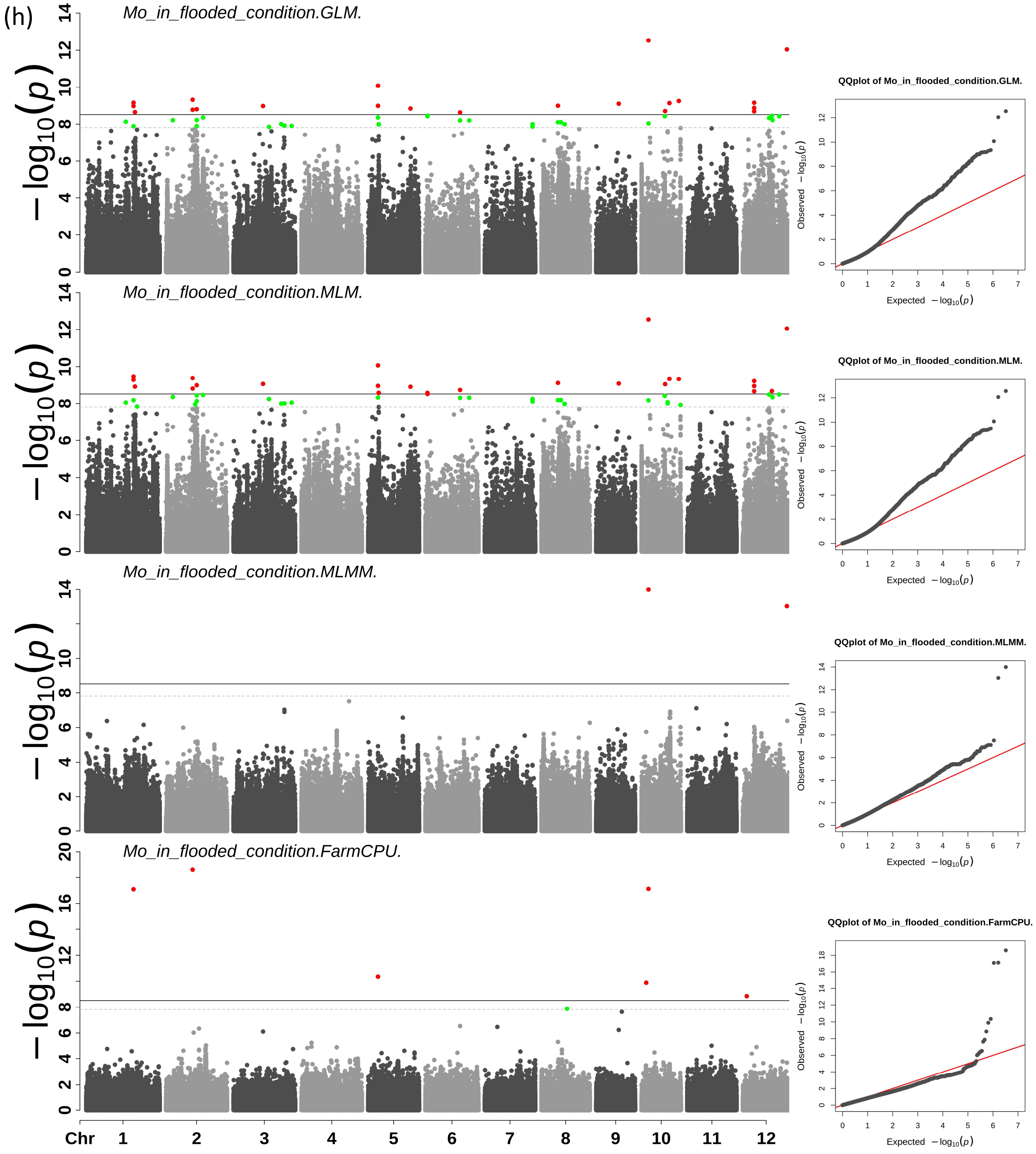
(f)



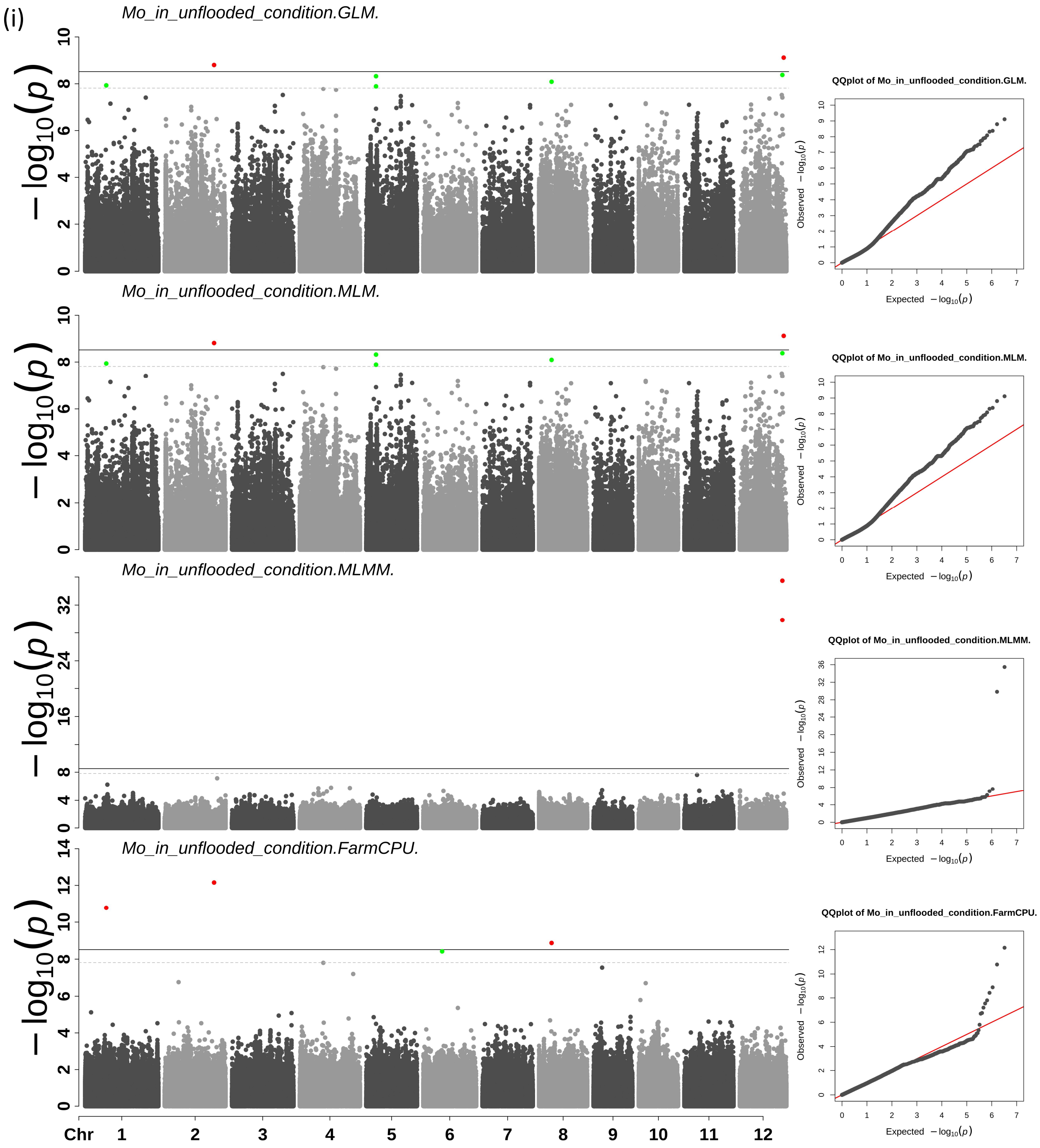
Supplementary Figure 2 (f) Genome-wide association analysis for Fe with GLM, MLM, MLMM, and FarmCPU methods (left) in unflooded condition. Quantile-quantile plot of each model (right). The horizontal dot grey line and green dots indicate the Bonferroni-corrected significance thresholds and SNPs at −log10(*P*) = 7.81. The horizontal solid grey line and red dots indicate the Bonferroni-corrected significance thresholds and SNPs at −log10(*P*) = 8.51.



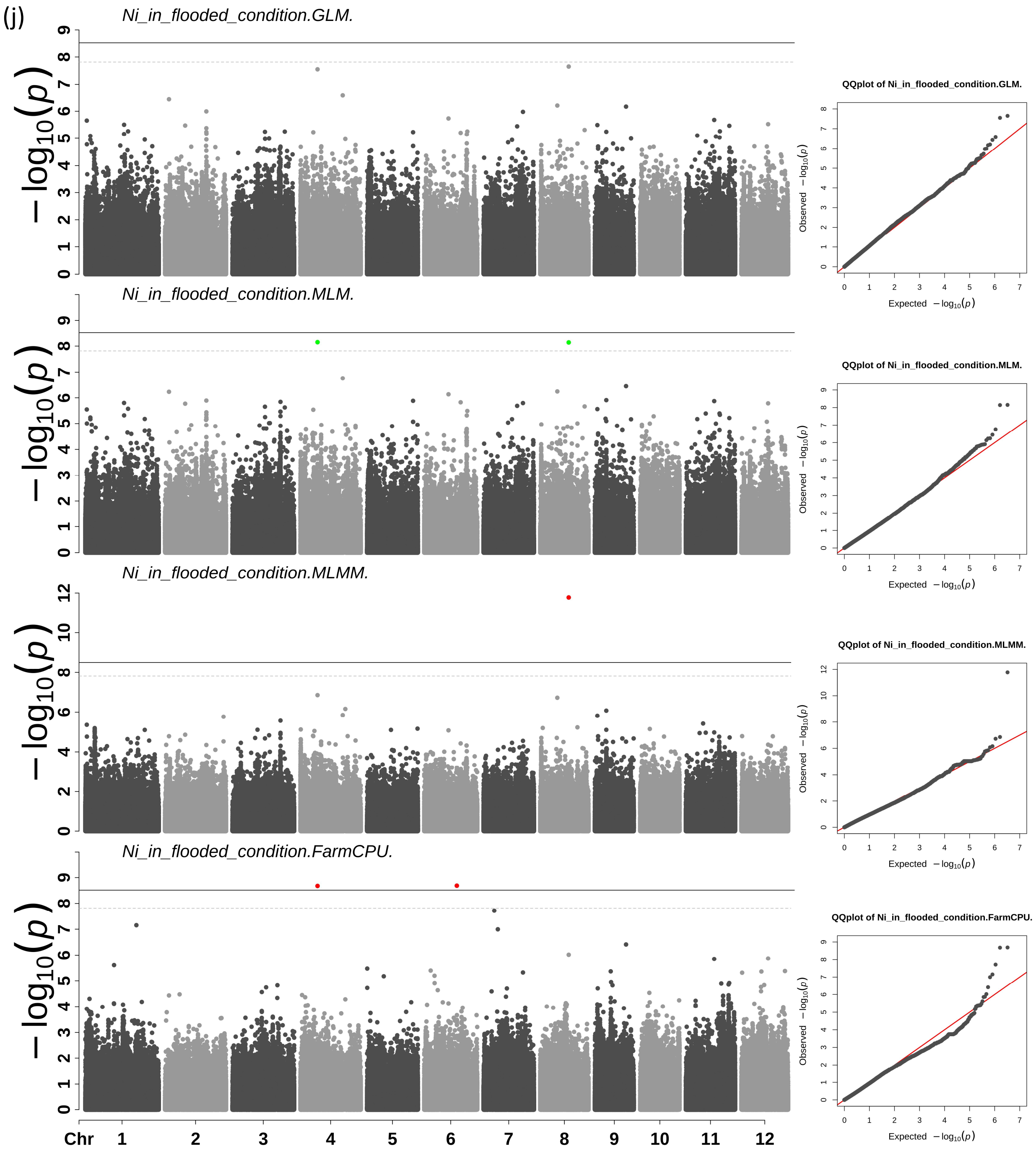
Supplementary Figure 2 (g) Genome-wide association analysis for K with GLM, MLM, MLMM, and FarmCPU methods (left) in flooded condition. Quantile-quantile plot of each model (right). The horizontal dot grey line and green dots indicate the Bonferroni-corrected significance thresholds and SNPs at −log10(*P*) = 7.81. The horizontal solid grey line and red dots indicate the Bonferroni-corrected significance thresholds and SNPs at −log10(*P*) = 8.51.



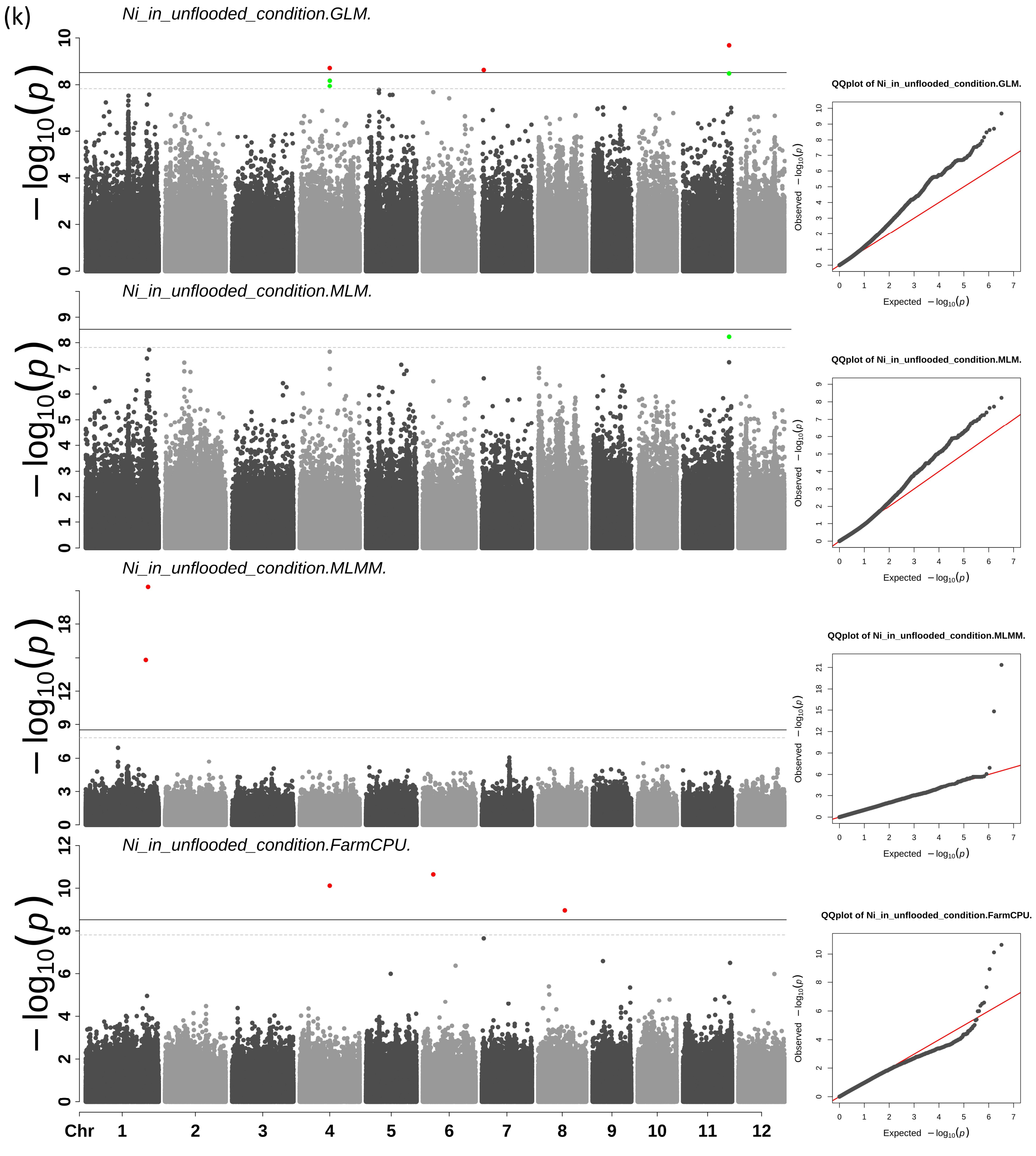
Supplementary Figure 2 (h) Genome-wide association analysis for Mo with GLM, MLM, MLMM, and FarmCPU methods (left) in flooded condition. Quantile-quantile plot of each model (right). The horizontal dot grey line and green dots indicate the Bonferroni-corrected significance thresholds and SNPs at $-\log10(P) = 7.81$. The horizontal solid grey line and red dots indicate the Bonferroni-corrected significance thresholds and SNPs at $-\log10(P) = 8.51$.



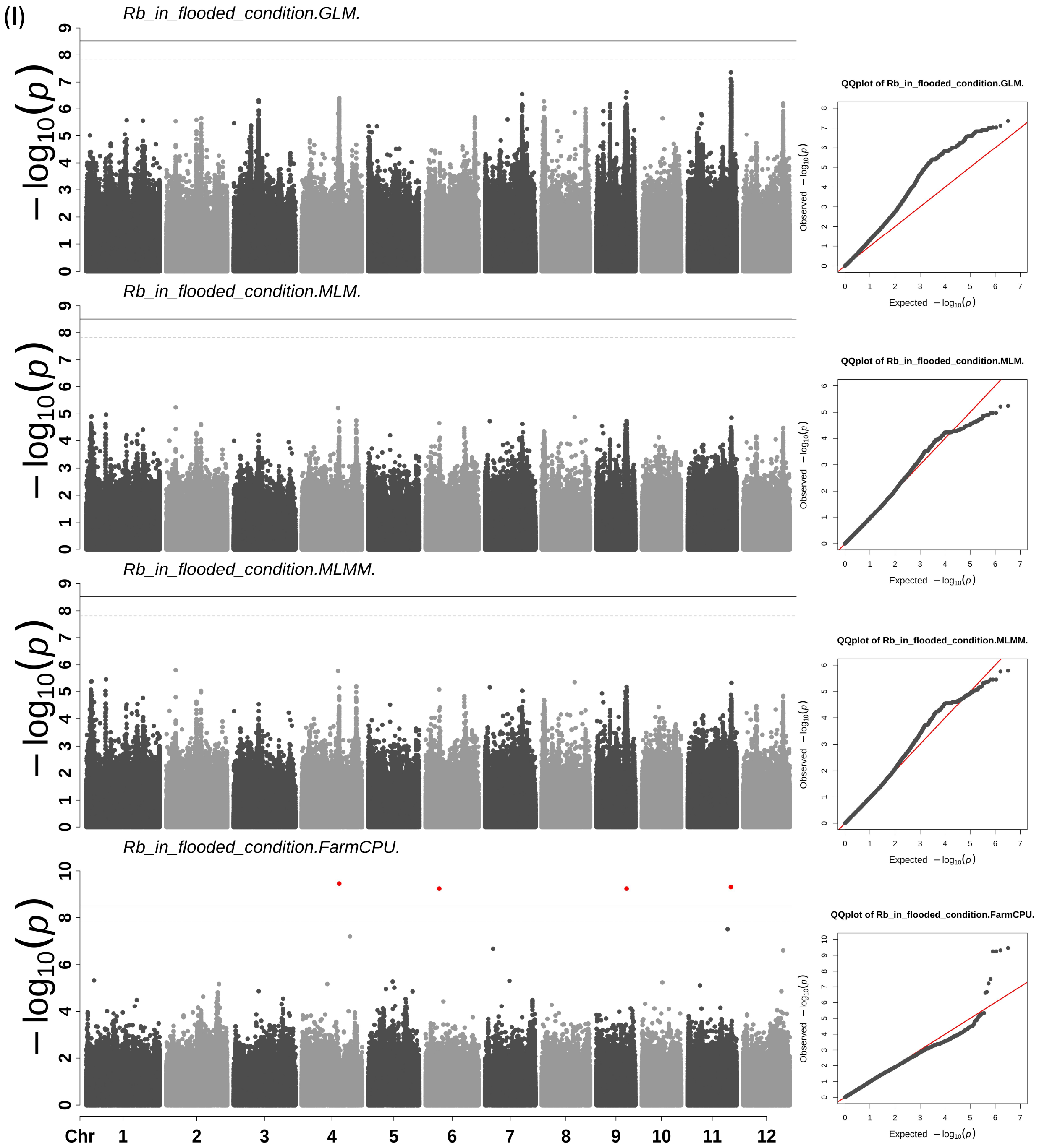
Supplementary Figure 2 (i) Genome-wide association analysis for Mo with GLM, MLM, MLMM, and FarmCPU methods (left) in unflooded condition. Quantile-quantile plot of each model (right). The horizontal dot grey line and green dots indicate the Bonferroni-corrected significance thresholds and SNPs at −log10(*P*) = 7.81. The horizontal solid grey line and red dots indicate the Bonferroni-corrected significance thresholds and SNPs at −log10(*P*) = 8.51.



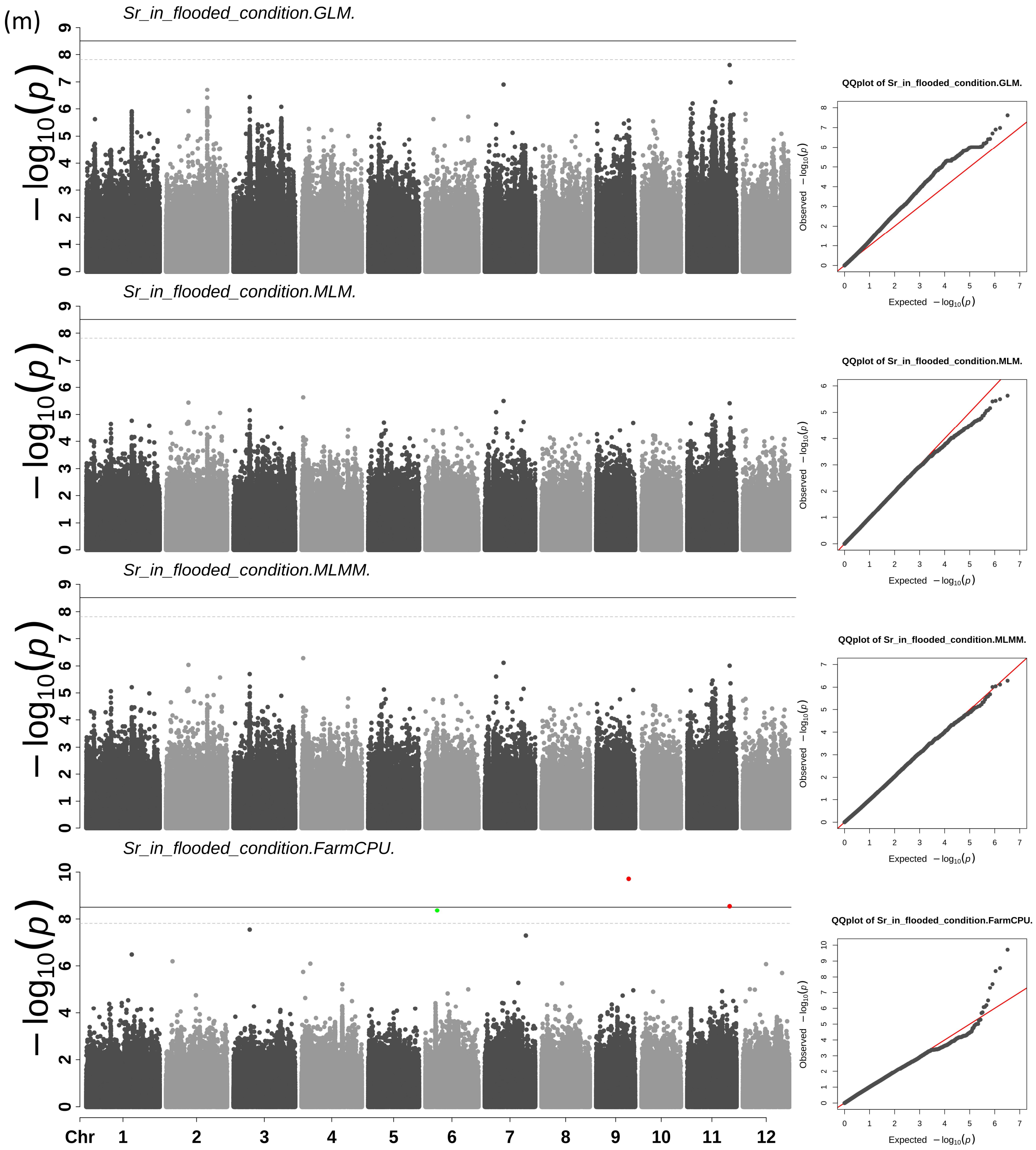
Supplementary Figure 2 (j) Genome-wide association analysis for Ni with GLM, MLM, MLMM, and FarmCPU methods (left) in flooded condition. Quantile-quantile plot of each model (right). The horizontal dot grey line and green dots indicate the Bonferroni-corrected significance thresholds and SNPs at −log10(*P*) = 7.81. The horizontal solid grey line and red dots indicate the Bonferroni-corrected significance thresholds and SNPs at −log10(*P*) = 8.51.



Supplementary Figure 2 (k) Genome-wide association analysis for Ni with GLM, MLM, MLMM, and FarmCPU methods (left) in unflooded condition. Quantile-quantile plot of each model (right). The horizontal dot grey line and green dots indicate the Bonferroni-corrected significance thresholds and SNPs at −log10(*P*) = 7.81. The horizontal solid grey line and red dots indicate the Bonferroni-corrected significance thresholds and SNPs at −log10(*P*) = 8.51.

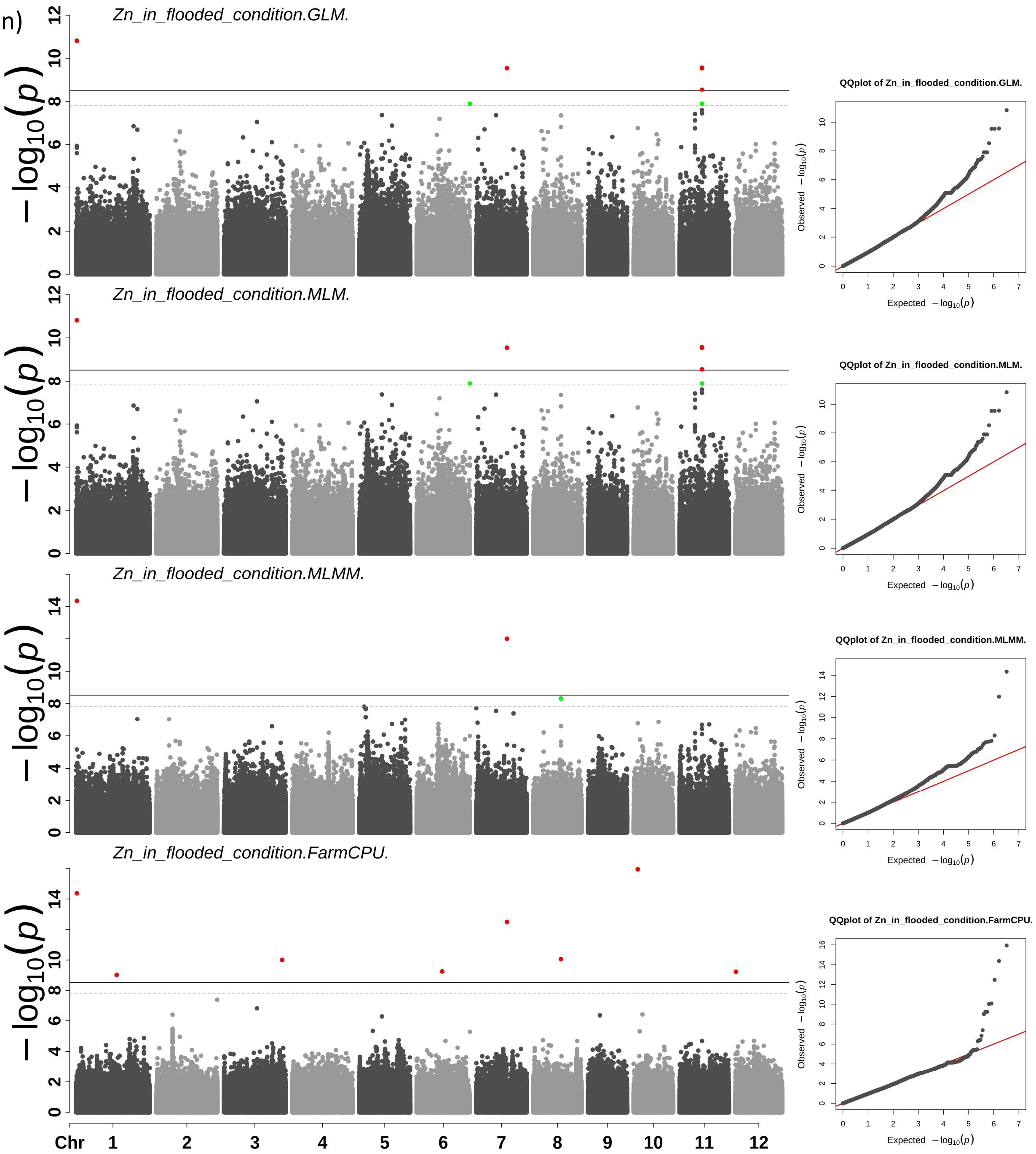


Supplementary Figure 2 (l) Genome-wide association analysis for Rb with GLM, MLM, MLMM, and FarmCPU methods (left) in flooded condition. Quantile-quantile plot of each model (right). The horizontal dot grey line and green dots indicate the Bonferroni-corrected significance thresholds and SNPs at −log10(*P*) = 7.81. The horizontal solid grey line and red dots indicate the Bonferroni-corrected significance thresholds and SNPs at −log10(*P*) = 8.51.

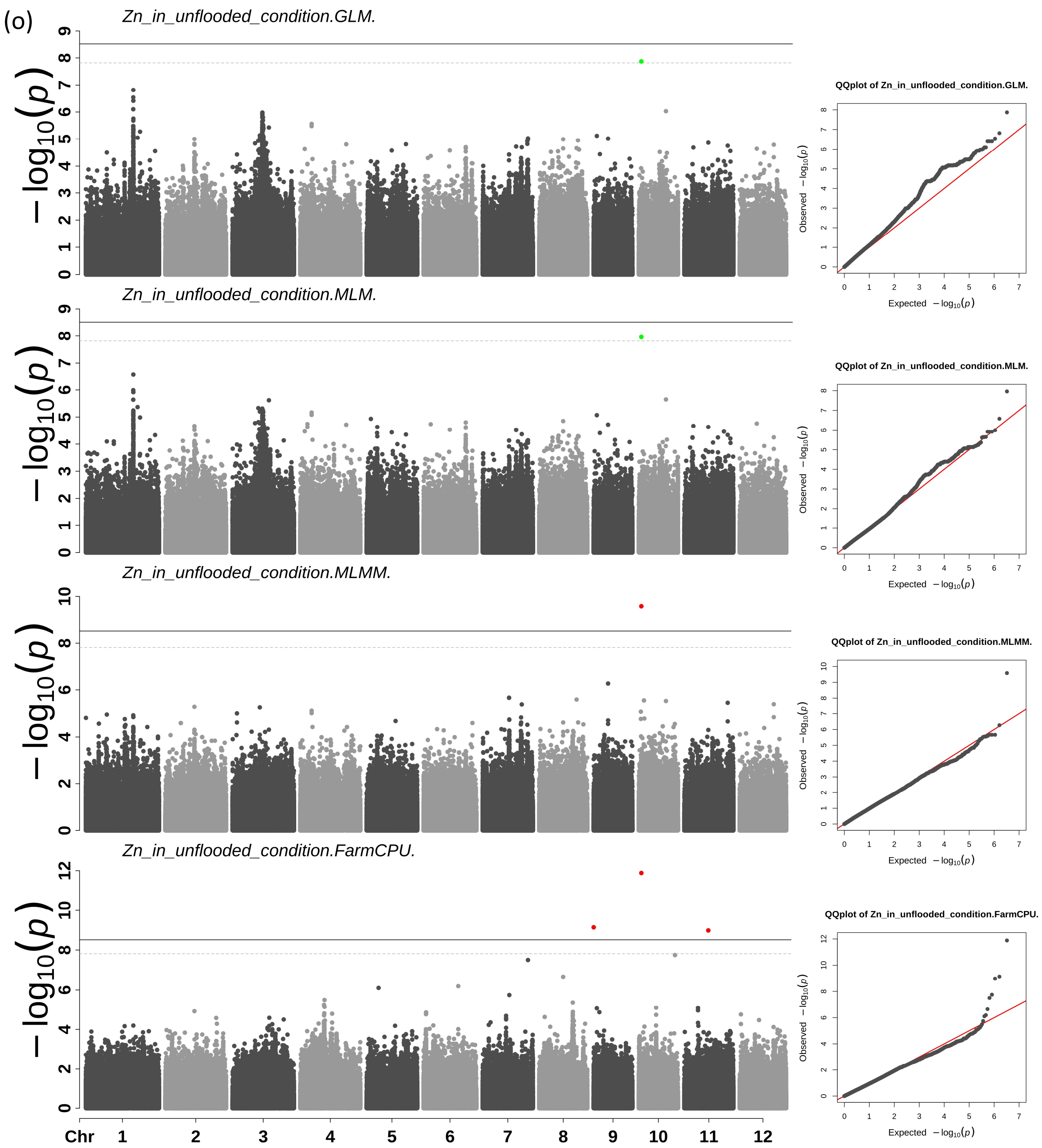


Supplementary Figure 2 (m) Genome-wide association analysis for Sr with GLM, MLM, MLMM, and FarmCPU methods (left) in flooded condition. Quantile-quantile plot of each model (right). The horizontal dot grey line and green dots indicate the Bonferroni-corrected significance thresholds and SNPs at −log10(*P*) = 7.81. The horizontal solid grey line and red dots indicate the Bonferroni-corrected significance thresholds and SNPs at −log10(*P*) = 8.51.

(n)



Supplementary Figure 2 (n) Genome-wide association analysis for Zn with GLM, MLM, MLMM, and FarmCPU methods (left) in flooded condition. Quantile-quantile plot of each model (right). The horizontal dot grey line and green dots indicate the Bonferroni-corrected significance thresholds and SNPs at −log10(*P*) = 7.81. The horizontal solid grey line and red dots indicate the Bonferroni-corrected significance thresholds and SNPs at −log10(*P*) = 8.51.



Supplementary Figure 2 (o) Genome-wide association analysis for Zn with GLM, MLM, MLMM, and FarmCPU methods (left) in unflooded condition. Quantile-quantile plot of each model (right). The horizontal dot grey line and green dots indicate the Bonferroni-corrected significance thresholds and SNPs at −log10(*P*) = 7.81. The horizontal solid grey line and red dots indicate the Bonferroni-corrected significance thresholds and SNPs at −log10(*P*) = 8.51.